

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/565,438  
Source: IFWP  
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IFWP

## RAW SEQUENCE LISTING

DATE: 08/11/2006

PATENT APPLICATION: US/10/565,438

TIME: 11:39:04

Input Set : A:\05101133.APP

Output Set: N:\CRF4\08112006\J565438.raw

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3 <110> APPLICANT: COSSON, BERTRAND
4     PAILLARD, LUC
5     LEGAGNEUX, VINCENT
6     OSBORNE, HOWARD
8 <120> TITLE OF INVENTION: PEPTIDE PROTEIN TRANSLATION INHIBITOR AND THE USE
9     THEREOF FOR PROTEIN TRANSLATION CONTROL
11 <130> FILE REFERENCE: 0510-1133
13 <140> CURRENT APPLICATION NUMBER: 10/565,438
14 <141> CURRENT FILING DATE: 2006-01-20
16 <150> PRIOR APPLICATION NUMBER: PCT/FR04/050345
17 <151> PRIOR FILING DATE: 2004-07-20
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: PatentIn Ver. 3.3
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24 <211> LENGTH: 28
25 <212> TYPE: PRT
26 <213> ORGANISM: Xenopus laevis
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32           20           25
33
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37 <211> LENGTH: 28
38 <212> TYPE: PRT
39 <213> ORGANISM: Homo sapiens
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45           20           25
46
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 84
51 <212> TYPE: PRT
52 <213> ORGANISM: Xenopus laevis
54 <400> SEQUENCE: 3
55 Phe Thr Thr Arg Ser Met Ala Gln Met Ala Ile Lys Ser Met His Gln
56   1           5           10           15
57 Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Ile Val Val Lys Phe Ala
58           20           25           30
59 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln
60           35           40           45
61 Gln Gln Met Gln Gln Leu Asn Ala Ala Ser Met Trp Gly Asn Leu Thr

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65      50      55      60
67 Gly Leu Asn Ser Leu Ala Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr
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70 Ala Ser Ser Gly
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75 <211> LENGTH: 88
76 <212> TYPE: PRT
77 <213> ORGANISM: Homo sapiens
79 <400> SEQUENCE: 4
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81 1      5      10      15
83 Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Met Val Val Lys Phe Ala
84      20      25      30
86 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Ala Gln Gln Leu Gln
87      35      40      45
89 Gln Gln Met Gln Gln Ile Ser Ala Ala Ser Val Trp Gly Asn Leu Ala
90      50      55      60
92 Gly Leu Asn Thr Leu Gly Pro Gln Tyr Leu Ala Leu Tyr Leu Gln Leu
93 65      70      75      80
95 Leu Gln Gln Thr Ala Ser Ser Gly
96      85
99 <210> SEQ ID NO: 5
100 <211> LENGTH: 189
101 <212> TYPE: PRT
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
106 fusion protein
108 <400> SEQUENCE: 5
109 Met Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Val Lys Phe Ala
110 1      5      10      15
112 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln
113      20      25      30
115 Gln Gln Met Gln Gln Leu Asn Ala Ala Ala Ala Met Ala Ser Asn Phe
116      35      40      45
118 Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr Gly Asp Val Thr Val
119      50      55      60
121 Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp Ile Ser Ser Asn
122 65      70      75      80
124 Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val Arg Gln Ser Ser
125      85      90      95
127 Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val Pro Lys Val Ala
128      100      105      110
130 Thr Gln Thr Val Gly Gly Glu Glu Leu Pro Val Ala Gly Trp Arg Ser
131      115      120      125
133 Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala Thr Asn Ser Asp
134      130      135      140
136 Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu Lys Asp Gly Asn
137 145      150      155      160

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139 Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile Tyr Gly Gly Gly
140           165           170           175
142 Gly Gly Ser Gly Pro Tyr Ser Ile Val Ser Pro Lys Cys
143           180           185
146 <210> SEQ ID NO: 6
147 <211> LENGTH: 154
148 <212> TYPE: PRT
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
153     fusion protein
155 <400> SEQUENCE: 6
156 Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
157   1           5           10           15
159 Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
160           20           25           30
162 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
163           35           40           45
165 Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
166           50           55           60
168 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Glu Glu Leu Pro Val
169   65           70           75           80
171 Ala Gly Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
172           85           90           95
174 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
175           100          105          110
177 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
178           115          120          125
180 Ile Tyr Gly Gly Gly Gly Gly Ser Lys Leu Gly Ser Met Ala Tyr Pro
181           130          135          140
183 Tyr Asp Val Pro Asp Tyr Ala Arg Ala Ala
184 145           150
187 <210> SEQ ID NO: 7
188 <211> LENGTH: 570
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
194     fusion polynucleotide
196 <400> SEQUENCE: 7
197 atggccttacc catacgatgt tccagattac gctagcgtaa agttcgcaga cactcagaaa 60
198 gacaaagaac agaagcgcac gacgcagcaa cttcagcagc aaatgcagca gctcaatgca 120
199 gcggccgcga tggcttctaa ctttactcag ttcgttctcg tcgacaatgg cggaactggc 180
200 gacgtgactg tcgcccgaag caacttcgct aacgggggtcg ctgaatggat cagctctaac 240
201 tcgcgatcac aggccttaca agtaacctgt agcggttcgtc agagctctgc gcagaatcgc 300
202 aaatacacca tcaaagtcga ggtgcctaaa gtggcaacc agactgttgg tggatgaagc 360
203 cttcctgtag ccggatggag atcttactta aatatggaac taaccattcc aattttcgcc 420
204 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480
205 ccgattccct cggccatcgc ggccaactcc ggcattctac gaggtggagg tggatctggg 540

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## RAW SEQUENCE LISTING

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206 ccctattcta tagtgtcacc taaatgctag 570
209 <210> SEQ ID NO: 8
210 <211> LENGTH: 570
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
216 fusion polynucleotide
218 <400> SEQUENCE: 8
219 atggccttacc catacgatgt tccagattac gctagcgtaa aatttgctga tacacagaag 60
220 gacaaagaac agaagagaat ggcccagcag ctccagcagc agatgcagca aatcagcgca 120
221 gcggccgcga tggcttctaa ctttactcag ttcgttctcg tcgacaatgg cggaactggc 180
222 gacgtgactg tcgcccacaag caacttcgct aacgggggtcg ctgaatggat cagctctaac 240
223 tcgcgatcac aggccttaca agtaacctgt agcgttcgtc agagctctgc gcagaatcgc 300
224 aaatacacca tcaaagtcga ggtgcctaaa gtggcaaccc agactgttgg tggatgaagag 360
225 cttcctgtag ccggatggag atcttactta aatatggaac taaccattcc aattttcgcc 420
226 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480
227 ccgattccct cggccatcgc ggccaactcc ggcattctac gaggtggagg tggatctggg 540
228 ccctattcta tagtgtcacc taaatgctag 570
231 <210> SEQ ID NO: 9
232 <211> LENGTH: 489
233 <212> TYPE: PRT
234 <213> ORGANISM: Xenopus laevis
236 <400> SEQUENCE: 9
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238 1 5 10 15
240 Lys Met Phe Val Gly Gln Val Pro Arg Ser Trp Ser Glu Lys Glu Leu
241 20 25 30
243 Arg Glu Leu Phe Glu Gln Tyr Gly Ala Val Tyr Glu Ile Asn Val Leu
244 35 40 45
246 Arg Asp Arg Ser Gln Asn Pro Pro Gln Ser Lys Gly Cys Cys Phe Ile
247 50 55 60
249 Thr Phe Tyr Thr Arg Lys Ala Ala Leu Glu Ala Gln Asn Ala Leu His
250 65 70 75 80
252 Asn Met Lys Val Leu Pro Gly Met His His Pro Ile Gln Met Lys Pro
253 85 90 95
255 Ala Asp Ser Glu Lys Asn Asn Ala Val Glu Asp Arg Lys Leu Phe Ile
256 100 105 110
258 Gly Met Val Ser Lys Asn Cys Asn Glu Asn Asp Ile Arg Ala Met Phe
259 115 120 125
261 Ser Pro Phe Gly Gln Ile Glu Glu Cys Arg Ile Leu Arg Gly Pro Asp
262 130 135 140
264 Gly Met Ser Arg Gly Cys Ala Phe Val Thr Phe Thr Thr Arg Ser Met
265 145 150 155 160
267 Ala Gln Met Ala Ile Lys Ser Met His Gln Ala Gln Thr Met Glu Gly
268 165 170 175
270 Cys Ser Ser Pro Ile Val Val Lys Phe Ala Asp Thr Gln Lys Asp Lys
271 180 185 190
273 Glu Gln Lys Arg Met Thr Gln Gln Leu Gln Gln Gln Met Gln Gln Leu

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274      195      200      205
276 Asn Ala Ala Ser Met Trp Gly Asn Leu Thr Gly Leu Asn Ser Leu Ala
277      210      215      220
279 Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr Ala Ser Ser Gly Asn Leu
280 225      230      235      240
282 Asn Ser Leu Ser Gly Leu His Pro Met Gly Ala Glu Tyr Gly Thr Gly
283      245      250      255
285 Met Thr Ser Gly Leu Asn Ala Ile Gln Leu Gln Asn Leu Ala Ala Leu
286      260      265      270
288 Ala Ala Ala Ser Ala Ala Gln Asn Thr Pro Ser Ala Gly Ala Ala
289      275      280      285
291 Leu Thr Ser Ser Ser Ser Pro Leu Ser Ile Leu Thr Ser Ser Gly Ser
292      290      295      300
294 Ser Pro Ser Ser Asn Asn Ser Ser Ile Asn Thr Met Ala Ser Leu Gly
295 305      310      315      320
297 Ala Leu Gln Thr Leu Ala Gly Ala Thr Ala Gly Leu Asn Val Asn Ser
298      325      330      335
300 Leu Ala Gly Met Ala Ala Phe Asn Gly Gly Leu Gly Ser Ser Leu Ser
301      340      345      350
303 Asn Gly Thr Gly Ser Thr Met Glu Ala Leu Ser Gln Ala Tyr Ser Gly
304      355      360      365
306 Ile Gln Gln Tyr Ala Ala Ala Ala Leu Pro Ser Leu Tyr Asn Gln Ser
307      370      375      380
309 Leu Leu Ser Gln Gln Gly Leu Gly Ala Ala Gly Ser Gln Lys Glu Gly
310 385      390      395      400
312 Pro Glu Gly Ala Asn Leu Phe Ile Tyr His Leu Pro Gln Glu Phe Gly
313      405      410      415
315 Asp Gln Asp Leu Leu Gln Met Phe Met Pro Phe Gly Asn Val Val Ser
316      420      425      430
318 Ser Lys Val Phe Ile Asp Lys Gln Thr Asn Leu Ser Lys Cys Phe Gly
319      435      440      445
321 Phe Val Ser Tyr Asp Asn Pro Val Ser Ala Gln Ala Ala Ile Gln Ser
322      450      455      460
324 Met Asn Gly Phe Gln Ile Gly Met Lys Arg Leu Lys Val Gln Leu Lys
325 465      470      475      480
327 Arg Ser Lys Asn Asp Ser Lys Pro Tyr
328      485
331 <210> SEQ ID NO: 10
332 <211> LENGTH: 1470
333 <212> TYPE: DNA
334 <213> ORGANISM: Xenopus laevis
336 <400> SEQUENCE: 10
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338 ggtcagggttc ctggaagctg gtcagagaaa gagctaagag aactcttcga gcagtacgga 120
339 gccgtctatg aaattaatgt tctccgagac agaagccaga atcctcctca gagcaaagga 180
340 tgctgtttta ttactttcta cacaagaaaa gctgcgtag aagcacagaa tgctttgcac 240
341 aacatgaaag ttctccctgg gatgcatcat ccaatacaga tgaagccagc cgacagtgaa 300
342 aagaataatg ctgtggaaga ccgaaagcta tttatcgga tggtttccaa gaattgtaat 360
343 gagaatgata tccgggccat gttctctccg tttggacaga tagaggaatg tcgtatcctg 420

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VERIFICATION SUMMARY

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